

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: 30-Jun-1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conley, Deirdre L.
- (B) REGISTRATION NUMBER: 36,487
- (C) REFERENCE/DOCKET NUMBER: P1084R1-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-2066
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2538 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mouse NRG3 nucleic acid
- (B) LOCATION: 1-2538
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50
TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
GCCCCGCGCC GCGCCCGCGC CCGGCCCGCG CGGCCCATG CCTCTGGCGC 250
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GCGGCGGGCG GCGGGGGGCC 400
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCGGA GTTACGCTGT 450
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGTTGT GCGTGGTGCC 500
TCTGTTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCCACGGA CCTGGTGGAC 600
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
CCGGGTTCCT ATCCGGGCTA GCGCGGCTC TACCACAGCA CGGAACACTG 850
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900
ACGCCCCGGT CCGGACCCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
TCCTCCTCAC CCTCTCCAC CTCCTCCACT ACCACCACCC CAGAACTAG 1100
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200

GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTCAT GTATCATCTT 1400
TGGAATTGTC ATCGTGGGCA TGTTCCTGTGC AGCATTCTAC TTCAAAAGCA 1450
AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
GAGCCATGTC CATCTACAAA ATTATTCAA GCGGATAGG CATCCTGTGA 1600
CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTT 1650
CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
CCCAGGACAA AGGAGTGGGA TGTTCATAG GAATACTTTC AGAAGGGCAC 1750
CACCCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
CAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACCTC 2150
CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
GTCCACGGC CAAATCAGAA CGAGAGGCAC AATTGTCTT AAGAAATGAA 2400
ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
(B) LOCATION: 1-713
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5				10						15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20				25						30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35				40						45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50				55						60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65				70						75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80				85						90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95				100						105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110				115						120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125				130						135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140				145						150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155				160						165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170				175						180	

Ser	Thr	Thr	Ala	Arg 185	Asn	Thr	Ala	Ala	Pro 190	Pro	Thr	Val	Leu	Ser 195
Thr	Thr	Ala	Pro	Phe 200	Phe	Ser	Ser	Ser	Thr 205	Pro	Gly	Ser	Arg	Pro 210
Pro	Met	Pro	Gly	Ala 215	Pro	Ser	Thr	Gln	Ala 220	Met	Pro	Ser	Trp	Pro 225
Thr	Ala	Ala	Tyr	Ala 230	Thr	Ser	Ser	Tyr	Leu 235	His	Asp	Ser	Thr	Pro 240
Ser	Trp	Thr	Leu	Ser 245	Pro	Phe	Gln	Asp	Ala 250	Ala	Ala	Ala	Ser	Ser 255
Ser	Ser	Pro	Ser	Ser 260	Thr	Ser	Ser	Thr	Thr 265	Thr	Thr	Pro	Glu	Thr 270
Ser	Thr	Ser	Pro	Lys 275	Phe	His	Thr	Thr	Thr 280	Tyr	Ser	Thr	Glu	Arg 285
Ser	Glu	His	Phe	Lys 290	Pro	Cys	Arg	Asp	Lys 295	Asp	Leu	Ala	Tyr	Cys 300
Leu	Asn	Asp	Gly	Glu 305	Cys	Phe	Val	Ile	Glu 310	Thr	Leu	Thr	Gly	Ser 315
His	Lys	His	Cys	Arg 320	Cys	Lys	Glu	Gly	Tyr 325	Gln	Gly	Val	Arg	Cys 330
Asp	Gln	Phe	Leu	Pro 335	Lys	Thr	Asp	Ser	Ile 340	Leu	Ser	Asp	Pro	Thr 345
Asp	His	Leu	Gly	Ile 350	Glu	Phe	Met	Glu	Ser 355	Glu	Asp	Val	Tyr	Gln 360
Arg	Gln	Val	Leu	Ser 365	Ile	Ser	Cys	Ile	Ile 370	Phe	Gly	Ile	Val	Ile 375
Val	Gly	Met	Phe	Cys 380	Ala	Ala	Phe	Tyr	Phe 385	Lys	Ser	Lys	Lys	Gln 390
Ala	Lys	Gln	Ile	Gln 395	Glu	His	Leu	Lys	Glu 400	Ser	Gln	Asn	Gly	Lys 405
Asn	Tyr	Ser	Leu	Lys 410	Ala	Ser	Ser	Thr	Lys 415	Ser	Glu	Ser	Leu	Met 420
Lys	Ser	His	Val	His 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Ala	Asp	Arg	His 435

Pro Val Thr Ala	Leu Glu Lys Ile Met	Glu Ser Ser Phe Ser	Ala
	440	445	450
Pro Gln Ser Phe	Pro Glu Val Thr Ser	Pro Asp Arg Gly Ser	Gln
	455	460	465
Pro Ile Lys His	His Ser Pro Gly Gln	Arg Ser Gly Met Leu	His
	470	475	480
Arg Asn Thr Phe	Arg Arg Ala Pro Pro	Ser Pro Arg Ser Arg	Leu
	485	490	495
Gly Gly Ile Val	Gly Pro Ala Tyr Gln	Gln Leu Glu Glu Ser	Arg
	500	505	510
Ile Pro Asp Gln	Asp Thr Ile Pro Cys	Gln Gly Ile Glu Val	Arg
	515	520	525
Lys Thr Ile Ser	His Leu Pro Ile Gln	Leu Trp Cys Val Glu	Arg
	530	535	540
Pro Leu Asp Leu	Lys Tyr Val Ser Asn	Gly Leu Arg Thr Gln	Gln
	545	550	555
Asn Ala Ser Ile	Asn Met Gln Leu Pro	Ser Arg Glu Thr Asn	Pro
	560	565	570
Tyr Phe Asn Ser	Leu Asp Gln Lys Asp	Leu Val Gly Tyr Leu	Ser
	575	580	585
Pro Arg Ala Asn	Ser Val Pro Ile Ile	Pro Ser Met Gly Leu	Glu
	590	595	600
Glu Thr Cys Met	Gln Met Pro Gly Ile	Ser Asp Val Lys Ser	Ile
	605	610	615
Lys Trp Cys Lys	Asn Ser Tyr Ser Ala	Asp Ile Val Asn Ala	Ser
	620	625	630
Met Pro Val Ser	Asp Cys Leu Leu Glu	Glu Gln Gln Glu Val	Lys
	635	640	645
Ile Leu Leu Glu	Thr Val Gln Glu Gln	Ile Arg Ile Leu Thr	Asp
	650	655	660
Ala Arg Arg Ser	Glu Asp Phe Glu Leu	Ala Ser Met Glu Thr	Glu
	665	670	675
Asp Ser Ala Ser	Glu Asn Thr Ala Phe	Leu Pro Leu Ser Pro	Thr
	680	685	690

Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile
695 700 705

Gln Arg Asp Ser Val Leu Thr Lys
710 713

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro				

[illegible]

(2) INFORMATION FOR SEQ ID NO:4:

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn
1 5 10 15
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys
20 25 30
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln
35 40 45
Phe Leu
47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
- (B) LOCATION: 1-2502
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50
GAGCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100
GCCGCGGCCC TCGGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150
AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200
TCGGCCGAGG AGGGCACCGC GCGGGCTGCG GCGGCGGCAG CGGCGGGCGG 250
GGGCCCCGAC GCGGGCGGCG AAGGGGCGGC CGAGCCCCCC CGGGAGTTAC 300
GCTGTAGCGA CTGCATCGTG TGAACCGGC AGCAGACGTG GCTGTGCGTG 350
GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400

CAAATGGATC	GTGGTGGGCT	CCGTCAAGGA	GTACGTGCCC	ACCGACCTAG	450	
TGGA	CTCCAA	GGGGATGGGC	CAGGACCCCT	TCTTCCTCTC	CAAGCCCAGC	500
TCTTTCCCCA	AGGCCATGGA	GACCACCACC	ACTACCACTT	CCACCACGTC	550	
CCCCGCCACC	CCCTCCGCCG	GGGGTGCCGC	CTCCTCCAGG	ACGCCCAACC	600	
GGATTAGCAC	TCGCCTGACC	ACCATCACGC	GGGCGCCCAC	TCGCTTCCCC	650	
GGGCACCGGG	TGCCCATCCG	GGCCAGCCCG	CGCTCCACCA	CAGCACGGAA	700	
CACTGCGGCC	CCTGCGACGG	TCCCGTCCAC	CACGGCCCCG	TTCTTCAGTA	750	
GCAGCACGCT	GGGCTCCCGA	CCCCCGGTGC	CAGGA	ACTCC	AAGTACCCAG	800
GCAATGCCCT	CCTGGCCTAC	TGCGGCATAC	GCTACCTCCT	CCTACCTTCA	850	
CGATTCTACT	CCCTCCTGGA	CCCTGTCTCC	CTTTCAGGAT	GCTGCCTCCT	900	
CTTCTTCCTC	TTCTTCCTCC	TCCGCTACCA	CCACCACACC	AGAAACTAGC	950	
ACCAGCCCCA	AATTTTCATAC	GACGACATAT	TCCACAGAGC	GATCCGAGCA	1000	
CTTCAAACCC	TGCCGAGACA	AGGACCTTGC	ATACTGTCTC	AATGATGGCG	1050	
AGTGCTTTGT	GATCGAAACC	CTGACCGGAT	CCCATAAACA	CTGTGCGTGC	1100	
AAAGAAGGCT	ACCAAGGAGT	CCGTTGTGAT	CAATTTCTGC	CGAAAACTGA	1150	
TTCCATCTTA	TCGGATCCAA	CAGACCACTT	GGGGATTGAA	TTCATGGAGA	1200	
GTGAAGAAGT	TTATCAAAGG	CAGGTGCTGT	CAATTTTCATG	TATCATCTTT	1250	
GGAATTGTCA	TCGTGGGCAT	GTTCTGTGCA	GCATTCTACT	TCAAAAGCAA	1300	
GAAACAAGCT	AAACAAATCC	AAGAGCAGCT	GAAAGTGCCA	CAAAATGGTA	1350	
AAAGCTACAG	TCTCAAAGCA	TCCAGCACAA	TGGCAAAGTC	AGAGAACTTG	1400	
GTGAAGAGCC	ATGTCCAGCT	GCAAAATTAT	TCAAAGGTGG	AAAGGCATCC	1450	
TGTGACTGCA	TTGGAGAAAA	TGATGGAGTC	AAGTTTTGTC	GGCCCCCAGT	1500	
CATTCCCTGA	GGTCCCTTCT	CCTGACAGAG	GAAGCCAGTC	TGTCAAACAC	1550	
CACAGGAGTC	TATCCTCTTG	CTGCAGCCCA	GGGCAAAGAA	GTGGCATGCT	1600	
CCATAGGAAT	GCCTTCAGAA	GGACACCCCC	GTCACCCCGA	AGTAGGCTAG	1650	
GTGGAATTGT	GGGACCAGCA	TATCAGCAAC	TCGAAGAATC	AAGGATCCCA	1700	

Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala		20	25	30
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala		35	40	45
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp		50	55	60
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly		65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val		80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser		95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser		110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr		125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr		140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro		155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg		170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser		185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro		200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro		215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro		230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser		245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr		260	265	270

Ser	Pro	Lys	Phe	His 275	Thr	Thr	Thr	Tyr	Ser 280	Thr	Glu	Arg	Ser	Glu 285
His	Phe	Lys	Pro	Cys 290	Arg	Asp	Lys	Asp	Leu 295	Ala	Tyr	Cys	Leu	Asn 300
Asp	Gly	Glu	Cys	Phe 305	Val	Ile	Glu	Thr	Leu 310	Thr	Gly	Ser	His	Lys 315
His	Cys	Arg	Cys	Lys 320	Glu	Gly	Tyr	Gln	Gly 325	Val	Arg	Cys	Asp	Gln 330
Phe	Leu	Pro	Lys	Thr 335	Asp	Ser	Ile	Leu	Ser 340	Asp	Pro	Thr	Asp	His 345
Leu	Gly	Ile	Glu	Phe 350	Met	Glu	Ser	Glu	Glu 355	Val	Tyr	Gln	Arg	Gln 360
Val	Leu	Ser	Ile	Ser 365	Cys	Ile	Ile	Phe	Gly 370	Ile	Val	Ile	Val	Gly 375
Met	Phe	Cys	Ala	Ala 380	Phe	Tyr	Phe	Lys	Ser 385	Lys	Lys	Gln	Ala	Lys 390
Gln	Ile	Gln	Glu	Gln 395	Leu	Lys	Val	Pro	Gln 400	Asn	Gly	Lys	Ser	Tyr 405
Ser	Leu	Lys	Ala	Ser 410	Ser	Thr	Met	Ala	Lys 415	Ser	Glu	Asn	Leu	Val 420
Lys	Ser	His	Val	Gln 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Val	Glu	Arg	His 435
Pro	Val	Thr	Ala	Leu 440	Glu	Lys	Met	Met	Glu 445	Ser	Ser	Phe	Val	Gly 450
Pro	Gln	Ser	Phe	Pro 455	Glu	Val	Pro	Ser	Pro 460	Asp	Arg	Gly	Ser	Gln 465
Ser	Val	Lys	His	His 470	Arg	Ser	Leu	Ser	Ser 475	Cys	Cys	Ser	Pro	Gly 480
Gln	Arg	Ser	Gly	Met 485	Leu	His	Arg	Asn	Ala 490	Phe	Arg	Arg	Thr	Pro 495
Pro	Ser	Pro	Arg	Ser 500	Arg	Leu	Gly	Gly	Ile 505	Val	Gly	Pro	Ala	Tyr 510
Gln	Gln	Leu	Glu	Glu 515	Ser	Arg	Ile	Pro	Asp 520	Gln	Asp	Thr	Ile	Pro 525

Cys	Gln	Gly	Ile	Glu	Val	Arg	Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	530	535	540
Gln	Leu	Trp	Cys	Val	Glu	Arg	Pro	Leu	Asp	Leu	Lys	Tyr	Ser	Ser	545	550	555
Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	Ser	Ile	Asn	Met	Gln	Leu	560	565	570
Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	Asn	Ser	Leu	Glu	Gln	Lys	575	580	585
Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	Ala	Ser	Ser	Val	Pro	Ile	590	595	600
Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: cARIA.egf
 (B) LOCATION: 1-48
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn
 1 5 10 15
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg
 20 25 30
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
 35 40 45
Asn Tyr Val
 48

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hAR.egf
 (B) LOCATION: 1-45
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
 1 5 10 15
Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
 20 25 30
Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hBTC.efg
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 5 10 15
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val
20 25 30
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hEGF.egf
(B) LOCATION: 1-46
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
20 25 30
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
35 40 45
Leu
46

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHB-EGF.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile
20 25 30
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHRGalpha.egf
(B) LOCATION: 1-49
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr
35 40 45
Glu Asn Tyr Pro
49

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His
1 5 10 15
Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val
20 25 30
Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mEPR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Ile Thr Lys Cys Ser Ser Asp Met Asp Gly Tyr Cys Leu His
1 5 10 15
Gly Gln Cys Ile Tyr Leu Val Asp Met Arg Glu Lys Phe Cys Arg
20 25 30
Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys Glu His Phe Phe Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Oligonucleotide probe
(B) LOCATION: 1-50
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly
1 5 10 15
Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly
20 25 30
Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys
35 40 45
Ala Gly Ala Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 1
- (B) LOCATION: 1-8
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Asp Gly Glu Cys Phe Val Ile
1 5 8

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 2
- (B) LOCATION: 1-9
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Phe Met Glu Ser Glu Glu Val Tyr
1 5 9

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: EST Genbank entry H23651
- (B) LOCATION: 1-466
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100
AATTTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150
CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTTNTGAT GACATTTNCA 400
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450
TTTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2091 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTTGCGCAGC 50
CGCCGCCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100
CGGGCGGGGG CCCGGACGGC GCGGCGGAAG GGGCGGCCGA GGGGGGGGG 150
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCACC 300
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCCAA 350
GCCCAGCTCT TTCCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450

AAACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAG CATCAAATGG 1800
 TGCAAAACT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850
 CGATTGTCTT ATAGCAGAAC AACAGAAGT GAAAATATTG CTAGAACTG 1900
 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950
 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGCGAAA ACACAGCCTT 2000
 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050
 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	

Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr
				125						130				135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr
				140					145					150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro
				155					160					165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg
				170					175					180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser
				185					190					195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro
				200					205					210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro
				215					220					225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro
				230					235					240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr
				260					265					270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu
				275					280					285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
				290					295					300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				305					310					315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				320					325					330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His
				335					340					345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln
				350					355					360
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly
				365					370					375

Met Phe Cys Ala	Ala Phe Tyr Phe Lys	Ser Lys Lys Gln Ala	Lys
380		385	390
Gln Ile Gln Glu	Gln Leu Lys Val Pro	Gln Asn Gly Lys Ser	Tyr
395		400	405
Ser Leu Lys Ala	Ser Ser Thr Met Ala	Lys Ser Glu Asn Leu	Val
410		415	420
Lys Ser His Val	Gln Leu Gln Asn Tyr	Ser Lys Val Glu Arg	His
425		430	435
Pro Val Thr Ala	Leu Glu Lys Met Met	Glu Ser Ser Phe Val	Gly
440		445	450
Pro Gln Ser Phe	Pro Glu Val Pro Ser	Pro Asp Arg Gly Ser	Gln
455		460	465
Ser Val Lys His	His Arg Ser Leu Ser	Ser Cys Cys Ser Pro	Gly
470		475	480
Gln Arg Ser Gly	Met Leu His Arg Asn	Ala Phe Arg Arg Thr	Pro
485		490	495
Pro Ser Pro Arg	Ser Arg Leu Gly Gly	Ile Val Gly Pro Ala	Tyr
500		505	510
Gln Gln Leu Glu	Glu Ser Arg Ile Pro	Asp Gln Asp Thr Ile	Pro
515		520	525
Cys Gln Gly Tyr	Ser Ser Ser Gly Leu	Lys Thr Gln Arg Asn	Thr
530		535	540
Ser Ile Asn Met	Gln Leu Pro Ser Arg	Glu Thr Asn Pro Tyr	Phe
545		550	555
Asn Ser Leu Glu	Gln Lys Asp Leu Val	Gly Tyr Ser Ser Thr	Arg
560		565	570
Ala Ser Ser Val	Pro Ile Ile Pro Ser	Val Gly Leu Glu Glu	Thr
575		580	585
Cys Leu Gln Met	Pro Gly Ile Ser Glu	Val Lys Ser Ile Lys	Trp
590		595	600
Cys Lys Asn Ser	Tyr Ser Ala Asp Val	Val Asn Val Ser Ile	Pro
605		610	615
Val Ser Asp Cys	Leu Ile Ala Glu Gln	Gln Glu Val Lys Ile	Leu
620		625	630

Leu	Glu	Thr	Val	Gln	Glu	Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	
				635					640					645	
Arg	Ser	Glu	Asp	Tyr	Glu	Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	
				650					655					660	
Ala	Ser	Glu	Asn	Thr	Ala	Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	
				665					670					675	
Ser	Glu	Arg	Glu	Ala	Gln	Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	
				680					685					690	
Asp	Ser	Ala	Leu	Thr	Lys										
				695	696										